```
RAW SEQUENCE LISTING              DATE: 06/04/2002
PATENT APPLICATION:  US/10/053,662A   TIME: 14:51:20

Input Set : A:\seqlisting.txt
Output Set: N:\CRF3\06042002\J053662A.raw
```

ENTERED

```
 4 <110> APPLICANT: Alexandra Charlesworth
 5         Falvia Spirito
 6         Guerrino Meneguzzi
 7         John Baird
 8         Keith Linder
10 <120> TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
11         HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
12         BULLOSA
14 <130> FILE REFERENCE: p84us4
16 <140> CURRENT APPLICATION NUMBER: US/10/053,662A
16 <141> CURRENT FILING DATE: 2002-01-24
16 <160> NUMBER OF SEQ ID NOS: 32
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 3989
22 <212> TYPE: DNA
23 <213> ORGANISM: equine
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (198)...(3767)
29 <223> OTHER INFORMATION:
31 <400> SEQUENCE: 1
32 tgggtcctcc ttattcacag gtgagtcaca ccctgaaaca caggctctct tcctgtcagg      60
33 actgagtcag gtagaagagt cgataaaacc acctgatcaa ggaaaaggaa ggcacagcgg     120
34 agcgcagagt gagaactccc agcggcgagg cgccgggcag cgacccctgc agcggcggac     180
35 cgcgcgccgg cctggcc atg cct gcg ctc tgg ctg agc tgc tac ctc tgc       230
36                     Met Pro Ala Leu Trp Leu Ser Cys Tyr Leu Cys
37                      1               5                   10
39 ttc tcg ctc ctc ctg ccc gca gcc cgg gcc acc tcc ggg agg gaa gtc      278
40 Phe Ser Leu Leu Leu Pro Ala Ala Arg Ala Thr Ser Gly Arg Glu Val
41          15                  20                  25
43 tgt gat tgc aac ggg aag tcc agg caa tgc atc ttt gac cag gaa ctt      326
44 Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys Ile Phe Asp Gln Glu Leu
45          30                  35                  40
47 cac aaa cag aca gga aat gga ttc cgc tgc ctc aac tgc aat gac aac      374
48 His Lys Gln Thr Gly Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn
49          45                  50                  55
51 act gat ggc atc cac tgc gag agg tgc aag gca gga ttt tac cga cag      422
52 Thr Asp Gly Ile His Cys Glu Arg Cys Lys Ala Gly Phe Tyr Arg Gln
53 60                  65                  70                  75
55 aga gaa agg gac cgc tgt tta ccc tgc aat tgt aac tct aaa ggt tct      470
56 Arg Glu Arg Asp Arg Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser
57          80                  85                  90
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59 ctt agc gct cga tgt gac aac tct gga cgg tgc agc tgt aag cca ggt      518
60 Leu Ser Ala Arg Cys Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly
61             95                  100                 105
63 gtg aca gga gac agg tgt gac cga tgt ctg ccc ggc ttc cac aca ctc      566
64 Val Thr Gly Asp Arg Cys Asp Arg Cys Leu Pro Gly Phe His Thr Leu
65             110                 115                 120
67 act gat gct ggg tgc gcc caa gac caa agg ctg cta gac tcc aag tgt      614
68 Thr Asp Ala Gly Cys Ala Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys
69     125                 130                 135
71 gac tgt gac cca gct ggc atc tca ggg ccc tgt gac tca ggc cgc tgt      662
72 Asp Cys Asp Pro Ala Gly Ile Ser Gly Pro Cys Asp Ser Gly Arg Cys
73 140                 145                 150                 155
75 gtc tgc aag ccg gct gtc act gga gag cgc tgt gat agg tgt cga cca      710
76 Val Cys Lys Pro Ala Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Pro
77             160                 165                 170
79 ggt tac tat cac ctg gat ggg gga aac cct cag ggc tgt acc cag tgt      758
80 Gly Tyr Tyr His Leu Asp Gly Gly Asn Pro Gln Gly Cys Thr Gln Cys
81             175                 180                 185
83 ttt tgc tat ggg cat tcc gcc agc tgc cac agc tct ggg gac tac agt      806
84 Phe Cys Tyr Gly His Ser Ala Ser Cys His Ser Ser Gly Asp Tyr Ser
85             190                 195                 200
87 gtc cat aaa atc atc tct gcc ttc cat caa gat gtt gat ggc tgg aag      854
88 Val His Lys Ile Ile Ser Ala Phe His Gln Asp Val Asp Gly Trp Lys
89     205                 210                 215
91 gct gtc caa aga aac ggg tct cct gca aag ctc cag tgg tca cag cgc      902
92 Ala Val Gln Arg Asn Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg
93 220                 225                 230                 235
95 cat cgg gat ata ttt agc tca gca cga cga tca gac cct gtc tat ttt      950
96 His Arg Asp Ile Phe Ser Ser Ala Arg Arg Ser Asp Pro Val Tyr Phe
97             240                 245                 250
99 gta gct cct gcc aaa ttt ctt ggg aat caa cag gtg agc tac ggg caa      998
100 Val Ala Pro Ala Lys Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln
101            255                 260                 265
103 agc cta tct ttt gac tac cgt gtg gat agg gga ggc aga cac cca tct     1046
104 Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser
105            270                 275                 280
107 gcc cat gac gtg atc ctg gaa ggt gct ggt cta cgg atc aca gct ccc     1094
108 Ala His Asp Val Ile Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro
109     285                 290                 295
111 ttg atg cca ctt agc aag aca ctg cct tgt ggg atc acc aag act tac     1142
112 Leu Met Pro Leu Ser Lys Thr Leu Pro Cys Gly Ile Thr Lys Thr Tyr
113 300                 305                 310                 315
115 aca ttc aga tta aat gaa cat cca agc agt aat tgg agc ccc cag cta     1190
116 Thr Phe Arg Leu Asn Glu His Pro Ser Ser Asn Trp Ser Pro Gln Leu
117             320                 325                 330
119 agt tac ttt gag tat cgg agg tta ctg cgg aac ctc aca gcc ctg cgg     1238
120 Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg
121             335                 340                 345
123 atc cga gct acc tac gga gaa tac agt act ggg tac att gac aac gtg     1286
```

```
124 Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val
125         350             355             360
127 acc ttg att tca gcc cgc ccc gtt tct gga gcc cca gcg ccc tgg gtt    1334
128 Thr Leu Ile Ser Ala Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val
129         365             370             375
131 gaa caa tgt gta tgc cct gtt ggc tac aag ggg cag ttc tgc cag gat    1382
132 Glu Gln Cys Val Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp
133 380             385             390             395
135 tgt gct tcc ggc tac aaa aga gat tca gcc aga ctg gga cct ttt ggc    1430
136 Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly
137             400             405             410
139 acc tgt att cca tgt aac tgc caa ggg gga ggg gcc tgc gat cca gac    1478
140 Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp
141             415             420             425
143 aca gga gac tgt tac tca ggg gat gag aac cct gac atc cct gag tgt    1526
144 Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Pro Glu Cys
145         430             435             440
147 gct gac tgc ccc att ggt ttc tac aac gat cca caa gac ccc cgc agc    1574
148 Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro Gln Asp Pro Arg Ser
149         445             450             455
151 tgc aag ccg tgc ccc tgt cgc aat ggg ttc agc tgc tcc gtg atg cct    1622
152 Cys Lys Pro Cys Pro Cys Arg Asn Gly Phe Ser Cys Ser Val Met Pro
153 460             465             470             475
155 gag aca gag gag gtg gtg tgc aat aac tgc ccc cag ggt gtc act ggt    1670
156 Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Gln Gly Val Thr Gly
157             480             485             490
159 gcc cgc tgt gag ctc tgt gct gat ggc tat ttt ggg gac ccc ttc ggg    1718
160 Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly
161             495             500             505
163 gaa cgt ggc cca gtg agg cct tgt cag ccc tgt cag tgc aac aac aac    1766
164 Glu Arg Gly Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn
165             510             515             520
167 gtg gac cct agt gcc tcc ggg aac tgt gac cgc ctg aca ggc agg tgt    1814
168 Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys
169         525             530             535
171 ctg aag tgc atc cac aac aca gct ggg gtc cac tgt gac cag tgc aaa    1862
172 Leu Lys Cys Ile His Asn Thr Ala Gly Val His Cys Asp Gln Cys Lys
173 540             545             550             555
175 gca ggc tac tat ggg gac ccg ttg gct ccc aat cca gca gac aag tgt    1910
176 Ala Gly Tyr Tyr Gly Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
177             560             565             570
179 cga gct tgc aac tgc aac cca gtg ggc tcg gag cct gtg gag tgt cga    1958
180 Arg Ala Cys Asn Cys Asn Pro Val Gly Ser Glu Pro Val Glu Cys Arg
181             575             580             585
183 agt gat ggc agc tgt gtt tgc aag cca ggc ttt ggt ggc ctc agc tgt    2006
184 Ser Asp Gly Ser Cys Val Cys Lys Pro Gly Phe Gly Gly Leu Ser Cys
185             590             595             600
187 gag cat gcg gca ctg acc agc tgt cca gct tgc tat aat caa gtg aag    2054
188 Glu His Ala Ala Leu Thr Ser Cys Pro Ala Cys Tyr Asn Gln Val Lys
```

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189      605                    610                    615
191 gtt cag atg gat cag ttt atg cag cag ctc cag atc ctg gag gcc ctg    2102
192 Val Gln Met Asp Gln Phe Met Gln Gln Leu Gln Ile Leu Glu Ala Leu
193 620                    625                    630                    635
195 att tcg aag gct cag ggt gga gca gta ccc aac gca gag ctg gaa ggc    2150
196 Ile Ser Lys Ala Gln Gly Gly Ala Val Pro Asn Ala Glu Leu Glu Gly
197                    640                    645                    650
199 agg atg cag cag gct gag cag gcc ctt cgg gac att ctg aga gaa gcc    2198
200 Arg Met Gln Gln Ala Glu Gln Ala Leu Arg Asp Ile Leu Arg Glu Ala
201                    655                    660                    665
203 cag att tca caa gat gct gtt aga tcc ttc aat ctc cgg gtg gcc aag    2246
204 Gln Ile Ser Gln Asp Ala Val Arg Ser Phe Asn Leu Arg Val Ala Lys
205            670                    675                    680
207 gca agg act caa gag aat agc tac cgg gac cgc ctg gat gac ctc aag    2294
208 Ala Arg Thr Gln Glu Asn Ser Tyr Arg Asp Arg Leu Asp Asp Leu Lys
209      685                    690                    695
211 atg act gtg gaa aga gtt cgg gcc ctg ggc agt cag tat cag aac caa    2342
212 Met Thr Val Glu Arg Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Gln
213 700                    705                    710                    715
215 gtt cag gat act cgc agg ctc atc act cag atg cgc ctg agc ctg gag    2390
216 Val Gln Asp Thr Arg Arg Leu Ile Thr Gln Met Arg Leu Ser Leu Glu
217                    720                    725                    730
219 gaa agt gag gct tcc ctg caa aac acc aac att cct cct tca gag cac    2438
220 Glu Ser Glu Ala Ser Leu Gln Asn Thr Asn Ile Pro Pro Ser Glu His
221                    735                    740                    745
223 tac gtg ggg cca aat ggc ttt aaa agt ctg gct cag gag gcc acg aga    2486
224 Tyr Val Gly Pro Asn Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg
225            750                    755                    760
227 ttg gca gac agc cat gtt cag tca gcc agt aac atg gag caa ctg gca    2534
228 Leu Ala Asp Ser His Val Gln Ser Ala Ser Asn Met Glu Gln Leu Ala
229      765                    770                    775
231 aag gaa acc cag gag tat tcc aaa gag ctg atg tca ctg gtg cgc gag    2582
232 Lys Glu Thr Gln Glu Tyr Ser Lys Glu Leu Met Ser Leu Val Arg Glu
233 780                    785                    790                    795
235 gct ctg cag gaa gga ggc gga agc ggc agc ctg gac gga gcc gtg gtg    2630
236 Ala Leu Gln Glu Gly Gly Gly Ser Gly Ser Leu Asp Gly Ala Val Val
237                    800                    805                    810
239 caa agg ctt gtg gga aaa ttg cag aaa act aaa tct ctg gcc cag gag    2678
240 Gln Arg Leu Val Gly Lys Leu Gln Lys Thr Lys Ser Leu Ala Gln Glu
241            815                    820                    825
243 ttg tcg agg gag gcc acg caa acc gac atg gaa gca gat agg tct tat    2726
244 Leu Ser Arg Glu Ala Thr Gln Thr Asp Met Glu Ala Asp Arg Ser Tyr
245            830                    835                    840
247 cag cat agt ctc cac ctt ctc aat tcc gtg tct cag att cag gga gtc    2774
248 Gln His Ser Leu His Leu Leu Asn Ser Val Ser Gln Ile Gln Gly Val
249      845                    850                    855
251 aat gat cag tcc ttg cag gta gaa gcg aag agg ctc aga caa aaa gct    2822
252 Asn Asp Gln Ser Leu Gln Val Glu Ala Lys Arg Leu Arg Gln Lys Ala
253 860                    865                    870                    875
```

```
255 gat tct ctc tca aac cgt gtg act aag cat atg gat gag ttc aag cac    2870
256 Asp Ser Leu Ser Asn Arg Val Thr Lys His Met Asp Glu Phe Lys His
257             880             885             890
259 gtg caa agc aat ctg gga aac tgg gaa gaa gaa acc cgg cag ctc tta    2918
260 Val Gln Ser Asn Leu Gly Asn Trp Glu Glu Glu Thr Arg Gln Leu Leu
261             895             900             905
263 cag aat gga aag aat ggg aga cag aca tca gat cag ctg ctt tcc cgt    2966
264 Gln Asn Gly Lys Asn Gly Arg Gln Thr Ser Asp Gln Leu Leu Ser Arg
265             910             915             920
267 gcc aac ctt gct aaa agc aga gcc caa gaa gca cta agt atg ggc aat    3014
268 Ala Asn Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn
269     925             930             935
271 gcc act ttt tat gaa gtt gag aac atc tta aag aat ctc aga gag ttt    3062
272 Ala Thr Phe Tyr Glu Val Glu Asn Ile Leu Lys Asn Leu Arg Glu Phe
273 940             945             950             955
275 gac ctg cag gtt gga gat aaa aga gca gaa gct gaa gag gcc atg aag    3110
276 Asp Leu Gln Val Gly Asp Lys Arg Ala Glu Ala Glu Glu Ala Met Lys
277             960             965             970
279 aga ctc tcc tac atc agc cag aag gtt gca ggt gcc agt gac aag acg    3158
280 Arg Leu Ser Tyr Ile Ser Gln Lys Val Ala Gly Ala Ser Asp Lys Thr
281             975             980             985
283 aag caa gca gaa gca gcc ctg ggc agt gct gct gcc gac gcc cag agg    3206
284 Lys Gln Ala Glu Ala Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg
285             990             995             1000
287 gca aag aat gca gcc agg gag gcc ctg gag atc tct ggc aag ata gaa    3254
288 Ala Lys Asn Ala Ala Arg Glu Ala Leu Glu Ile Ser Gly Lys Ile Glu
289     1005            1010            1015
291 cag gag ata gga ggt ctg aac ttg gaa gcc aat gtg aca gca gat gga    3302
292 Gln Glu Ile Gly Gly Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
293 1020            1025            1030            1035
295 gcc ttg gcc atg gag aag gga ctg gcc act ctg aaa agt gag atg aga    3350
296 Ala Leu Ala Met Glu Lys Gly Leu Ala Thr Leu Lys Ser Glu Met Arg
297             1040            1045            1050
299 gaa gtg gaa gga gag ctg tca agg aag gag cag gag ttt gac atg gat    3398
300 Glu Val Glu Gly Glu Leu Ser Arg Lys Glu Gln Glu Phe Asp Met Asp
301             1055            1060            1065
303 atg gac gca gtg cag atg gta att gca gag gcc caa aga gtt gaa aac    3446
304 Met Asp Ala Val Gln Met Val Ile Ala Glu Ala Gln Arg Val Glu Asn
305             1070            1075            1080
307 aga gcc aag aat gct gga gtt acg atc caa gac aca ctc aac aca ttg    3494
308 Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu
309     1085            1090            1095
311 gat ggc atc cta cac cta ata gac cag cct ggc agt gtg gat gaa gag    3542
312 Asp Gly Ile Leu His Leu Ile Asp Gln Pro Gly Ser Val Asp Glu Glu
313 1100            1105            1110            1115
315 agg ctg atc tta ctg gag cag aag ctt ttc cga gcc aag act cag atc    3590
316 Arg Leu Ile Leu Leu Glu Gln Lys Leu Phe Arg Ala Lys Thr Gln Ile
317             1120            1125            1130
319 aac agc cag cta cgg ccc ttg atg tca gag ctg gaa gag agg gca cat    3638
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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date